OIPE

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 1 <110> APPLICANT: Chadwick, Brian Paul
 2         Frischauf, Anna-Maria
 3 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
 4         POLYPEPTIDES AND NUCLEIC ACIDS
 5 <130> FILE REFERENCE: 9598-066
 6 <140> CURRENT APPLICATION NUMBER: 09/905,589
 7 <141> CURRENT FILING DATE: 2001-07-13
 9 <150> PRIOR APPLICATION NUMBER: US/09/240,639
10 <151> PRIOR FILING DATE: 1998-01-29
13 <160> NUMBER OF SEQ ID NOS: 29
14 <170> SOFTWARE: PatentIn Ver. 2.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 2762
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
20 <220> FEATURE:
21 <221> NAME/KEY: CDS
22 <222> LOCATION: (232)..(1599)
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26     gcgcggtgca tggaatgggc tatgtgaatg aaaaaaggta tccgttatga aacttccaga 180
27     aaaacgagct acattttca gcagccgcag cacggtcctt ggcaaacaag g atg aga 237
28                                                            Met Arg
29                                                              1
30     aaa ata tcc aac cac ggg agc ctg cgg gtg gcg aag gtg gca tac ccc 285
31     Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
32              5                  10                  15
33     ctg ggg ctg tgt gtg ggc gtg ttc atc tat gtt gcc tac atc aag tgg 333
34     Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
35          20                  25                  30
36     cac cgg gcc acc gcc acc cag gcc ttc ttc agc atc acc agg gca gcc 381
37     His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala
38      35                  40                  45                  50
39     ccg ggg gcc cgg tgg ggt cag cag gcc cac agc ccc ctg ggg aca gct 429
40     Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala
41                  55                  60                  65
42     gca gac ggg cac gag gtc ttc tac ggg atc atg ttt gat gca gga agc 477
43     Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser
44                  70                  75                  80
45     act ggc acc cga gta cac gtc ttc cag ttc acc cgg ccc ccc aga gaa 525
46     Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu
47                  85                  90                  95
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48   act ccc acg tta acc cac gaa acc ttc aaa gca gtg aag cca ggt ctt   573
49   Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu
50        100                105                110
51   tct gcc tat gct gat gat gtt gaa aag agc gct cag gga atc cgg gaa   621
52   Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu
53   115                120                125                130
54   cta ctg gat gtt gct aaa cag gac att ccg ttc gac ttc tgg aag gcc   669
55   Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala
56              135                140                145
57   acc cct ctg gtc ctc aag gcc aca gct ggc tta cgc ctg tta cct gga   717
58   Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly
59              150                155                160
60   gaa aag gcc cag aag tta ctg cag aag gtg aaa gaa gta ttt aaa gca   765
61   Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala
62              165                170                175
63   tcg cct ttc ctt gta ggg gat gac tgt gtt tcc atc atg aac gga aca   813
64   Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr
65              180                185                190
66   gat gaa ggc gtt tcg gcg tgg atc acc atc aac ttc ctg aca ggc agc   861
67   Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser
68   195                200                205                210
69   ttg aaa act cca gga ggg agc agc gtg ggc atg ctg gac ttg ggc gga   909
70   Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly
71              215                220                225
72   gga tcc act cag atc gcc ttc ctg cca cgc gtg gag ggc acc ctg cag   957
73   Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln
74              230                235                240
75   gcc tcc cca ccc ggc tac ctg acg gca ctg cgg atg ttt aac agg acc   1005
76   Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr
77              245                250                255
78   tac aag ctc tat tcc tac agc tac ctc ggg ctc ggg ctg atg tcg gca   1053
79   Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala
80              260                265                270
81   cgc ctg gcg atc ctg ggc ggc gtg gag ggg cag cct gct aag gat gga   1101
82   Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly
83   275                280                285                290
84   aag gag ttg gtc agc cct tgc ttg tct ccc agt ttc aaa gga gag tgg   1149
85   Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp
86              295                300                305
87   gaa cac gca gaa gtc acg tac agg gtt tca ggg cag aaa gca gcg gca   1197
88   Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala
89              310                315                320
90   agc ctg cac gag ctg tgt gct gcc aga gtg tca gag gtc ctt caa aac   1245
91   Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn
92              325                330                335
93   aga gtg cac agg acg gag gaa gtg aag cat gtg gac ttc tat gct ttc   1293
94   Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe
95   340                345                350
96   tcc tac tat tac gac ctt gca gct ggt gtg ggc ctc ata gat gcg gag   1341
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PATENT APPLICATION: US/09/905,589   TIME: 14:40:45

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 98        355                 360                 365                 370
 99        aag gga ggc agc ctg gtg gtg ggg gac ttc gag atc gca gcc aag tac  1389
100        Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr
101                        375                 380                 385
102        gtg tgt cgg acc ctg gag aca cag ccg cag agc agc ccc ttc tca tgc  1437
103        Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys
104                        390                 395                 400
105        atg gac ctc acc tac gtc agc ctg cta ctc cag gag ttc ggc ttt ccc  1485
106        Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro
107                        405                 410                 415
108        agg agc aaa gtg ctg aag ctc act cgg aaa att gac aat gtt gag acc  1533
109        Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr
110                 420                 425                 430
111        agc tgg gct ctg ggg gcc att ttt cat tac atc gac tcc ctg aac aga  1581
112        Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg
113        435                 440                 445                 450
114        cag aag agt cca gcc tca tagtggccga gccatccctg tccccgtcag          1629
115        Gln Lys Ser Pro Ala Ser
116                        455
117        cagtgtctgt gtgtctgcat aaaccctcct gtcctggacg tgacttcatc ctgaggagcc 1689
118        acagcacagg ccgtgctggc actttctgca cactggctct gggacttgca gaaggcctgg 1749
119        tgctgccctg gcatcagcct cttccagtca catctggcca gagggctgtc tggacctggg 1809
120        ccctgctcaa tgccacctgt ctgcctgggc tccaagtggg caggaccagg acagaaccac 1869
121        aggcacacac tgaggggggca gtgtggctcc ctgcctgtcc catccccatg ccccgtccgc 1929
122        ggggctgtgg ctgctgctgt gcatgtccct gcgatgggag tcttgtctcc cagcctgtca 1989
123        gtttcctccc cagggcagag ctcccccttcc tgcaagagtc tgggaggcgg tgcaggctgt 2049
124        cctggctgct ctggggaagc cgaggggacag ccataacacc cccgggacag taggtctggg 2109
125        cggcaccact gggaactctg gacttgagtg tgtttgctct tccttgggta tgaatgtgtg 2169
126        agttcacccca gaggcctgct ctcctcacac attgtgtggt ttggggttaa tgatggaggg 2229
127        agacacctct tcatagacgg caggtgccca cctttcaggg agtctcccag catgggcgga 2289
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129        gtgtgggtgc caagtgcttg tgtagaaact gtgttctgag ccccctttttc tggacaccaa 2409
130        ctgtgtcctg tgaatgtatc gctactgtga gctgttcccg cctagccagg gccatgtctt 2469
131        aggtgcagct gtgccacggg tcagctgagc cacagtccca gaaccaagct ctcggtgtct 2529
132        cgggccacca tccgcccacc tcgggctgac cccacctcct ccatggacag tgtgagcccc 2589
133        gggccgtgca tcctgctcag tgtggcgtca gtgtcggggc tgagcccctt gagctgcttc 2649
134        agtgaatgta cagtgcccgg cacgagctga acctcatgtg ttccactccc aataaaaggt 2709
135        tgacaggggc ttctccttca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa           2762
137 <210> SEQ ID NO: 2
138 <211> LENGTH: 456
139 <212> TYPE: PRT
140 <213> ORGANISM: Homo sapiens
141 <400> SEQUENCE: 2
142        Met Arg Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala
143        1               5                   10                  15
144        Tyr Pro Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile
145                        20                  25                  30
146        Lys Trp His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg
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149        50                    55                    60
150  Thr Ala Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala
151    65                    70                    75                    80
152  Gly Ser Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro
153                85                    90                    95
154  Arg Glu Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro
155              100                   105                   110
156  Gly Leu Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile
157             115                   120                   125
158  Arg Glu Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp
159       130                   135                   140
160  Lys Ala Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu
161  145                   150                   155                   160
162  Pro Gly Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe
163              165                   170                   175
164  Lys Ala Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn
165              180                   185                   190
166  Gly Thr Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr
167             195                   200                   205
168  Gly Ser Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu
169       210                   215                   220
170  Gly Gly Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr
171  225                   230                   235                   240
172  Leu Gln Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn
173              245                   250                   255
174  Arg Thr Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met
175              260                   265                   270
176  Ser Ala Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys
177       275                   280                   285
178  Asp Gly Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly
179       290                   295                   300
180  Glu Trp Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala
181  305                   310                   315                   320
182  Ala Ala Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu
183             325                   330                   335
184  Gln Asn Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr
185       340                   345                   350
186  Ala Phe Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp
187       355                   360                   365
188  Ala Glu Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala
189       370                   375                   380
190  Lys Tyr Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe
191  385                   390                   395                   400
192  Ser Cys Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly
193              405                   410                   415
194  Phe Pro Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val
195              420                   425                   430
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PATENT APPLICATION: US/09/905,589   DATE: 01/23/2002
                                      TIME: 14:40:45
Input Set : N:\Crf3\RULE60\09905589.raw
Output Set: N:\CRF3\01232002\I905589.raw

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198        Asn Arg Gln Lys Ser Pro Ala Ser
199            450                 455
201  <210> SEQ ID NO: 3
202  <211> LENGTH: 2797
203  <212> TYPE: DNA
204  <213> ORGANISM: Homo sapiens
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211        ctccgcacag ctaggagaaa ag atg ttc act gtg ctg acc cgc caa cca tgt  112
212                             Met Phe Thr Val Leu Thr Arg Gln Pro Cys
213                             1               5                   10
214        gag caa gca ggc ctc aag gcc ctc tac cga act cca acc atc att gcc  160
215        Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala
216                    15                  20                  25
217        ttg gtg gtc ttg ctt gtg agt att gtg gta ctt gtg agt atc act gtc  208
218        Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val
219                30                  35                  40
220        atc cag atc cac aag caa gag gtc ctc cct cca gga ctg aag tat ggt  256
221        Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly
222            45                  50                  55
223        att gtg ctg gat gcc ggg tct tca aga acc aca gtc tac gtg tat caa  304
224        Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln
225            60                  65                  70
226        tgg cca gca gaa aaa gag aat aat acc gga gtg gtc agt caa acc ttc  352
227        Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe
228        75                  80                  85                  90
229        aaa tgt agt gtg aaa ggc tct gga atc tcc agc tat gga aat aac ccc  400
230        Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro
231                        95                  100                 105
232        caa gat gtc ccc aga gcc ttt gag gag tgt atg caa aaa gtc aag ggg  448
233        Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly
234                    110                 115                 120
235        cag gtt cca tcc cac ctc cac gga tcc acc ccc att cac ctg gga gcc  496
236        Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala
237                125                 130                 135
238        acg gct ggg atg cgc ttg ctg agg ttg caa aat gaa aca gca gct aat  544
239        Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn
240            140                 145                 150
241        gaa gtc ctt gaa agc atc caa agc tac ttc aag tcc cag ccc ttt gac  592
242        Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp
243        155                 160                 165                 170
244        ttt agg ggt gct caa atc att tct ggg caa gaa gaa ggg gta tat gga  640
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1/23/02

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/905,589

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TIME: 14:40:47

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